REMARKS

The following Remarks address the issues presented in the Final Office Action in the order of their appearance:

Rejection of Claims 1-8, 10-12, 14-26, 28, and 29 Under §102(e) in View of Kamb (U.S. Patent No. 5,807,679):

This rejection is respectfully traversed because the Kamb patent describes a two-step process which is patentably distinct from the present claims. The passage at issue from the Kamb patent reads as follows (column 6, lines 48-56):

> A set of 30 primers is prepared. These primers are matched so that they will work equally well or nearly equally well under the single set of PCR conditions to be used. For example, they may be designed so each has a predicted Tm within a certain narrow range. The primers can be designed each to have a unique 5' sequence (**which will later be used as the primer for sequencing reactions**) and a degenerate 3' sequence **or the primers may simply be individual primers of arbitrary sequence**. (Emphasis added.)

The difference is that in the first step of the Kamb patent, the primers are not designed to amplify any particular region of the target. The primers are designed to amplify the target randomly. Note that the "unique 5' sequence" of the primers is utilized solely "as a primer" for subsequent sequencing reactions. The "unique 5' sequence" of Kamb's primers thus **does not** correspond to or complement any specific structure in the target. Nor does Kamb teach or suggest that rather than using the "unique 5' sequence" solely for subsequent sequencing, this portion could be used to specifically amplify a particular region within the target. In short, Kamb utilizes the "unique 5' sequence" of his primers solely to generate priming sites for subsequence sequencing.

In the present invention, however, the claims explicitly require that the first set of primars include a region of fixed sequence that is "identical to or complementary to" a consensus sequence of interest. This aspect of the invention simply is not taught or suggested by the Kamb patent.

Also, the present claims also require a second plurality of primers having an arbitrary region of fixed sequence and a randomized region. Note that Claim 1 explicitly requires, in step (c) that the nucleic acid template be amplified under conditions wherein the first set of primers binds to the consensus sequence of interest, while the second set of primers binds at at locations removed from the consensus sequence so that region between the first and second primers is "specifically" amplified.

This is different than Kamb's approach because in Kamb's approach **all** of the first set of primer bind randomly. Regardless of the configuration of Kamb's first set of primers, they are designed in an entirely arbitrary fashion. The "unique" portion of Kamb's primers is used solely to insert a sequencing primer location in the amplicons. Even so, Kamb's amplificons are entirely arbitrary. There is no attempt by Kamb to specifically amplify any distinct portion of the template that was selected in advance. Kamb's entire approach is focused solely on amplifying and sequencing unknown stretches of DNA, regardless of where they fall.

It is common knowledge that mammalian DNA contains large stretches of sequence that are uninformative. Rather than taking the time to amplify and sequence all of this uninformative DNA, which is Kamb's approach, the present invention targets only those portions of the DNA template that are of interest.

Thus, Applicants submit that the continued rejection of the claims in view of Kamb et al. is improper. Withdrawal of the same is respectfully requested.

CONCLUSION

Applicant respectfully submits that the application is now in condition for allowance. Early notification of such action is earnestly solicited.

Respectfully submitted,

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